

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1-4. (Canceled).

5. (Currently amended) A method of determining if a positionally-addressable biopolymer array has a synthesis defect, said method comprising the following steps in the order stated:

- a) contacting ~~the~~ a positionally-addressable biopolymer array of claim 1-2 with a sample, wherein said positionally addressable biopolymer array comprises a substrate to which are attached a plurality of different biopolymer probes, said different biopolymer probes being situated at different positions on said substrate and being the product of a step-by-step synthesis of said different biopolymer probes on said substrate, said plurality of different biopolymer probes comprising a plurality of quality control probes, each quality control probe in said plurality of quality control probes comprising (i) the same predetermined binding sequence or (ii) a different predetermined binding sequence with the same binding specificity, the synthesis of said predetermined binding sequence in each said quality control probe having been initiated during said step-by-step synthesis at sequential cycles of synthesis, wherein said sample comprises ~~comprising~~ a binding partner that binds said predetermined binding sequence;
- b) detecting or measuring binding between two or more of said quality control probes and said binding partner in the sample; and
- c) comparing binding of said two or more of said quality control probes, wherein if said binding is similar, the absence of a synthesis defect between said sequential cycles of synthesis of said array is indicated.

6. (Currently amended) A method of determining if a positionally-addressable biopolymer array has a synthesis defect, said method comprising the following steps in the order stated:

- a) contacting ~~the~~ a positionally-addressable biopolymer array of claim 3 with a sample, wherein said positionally addressable biopolymer array comprises a substrate to

which are attached a plurality of different biopolymer probes, said different biopolymer probes being situated at different positions on said substrate and being the product of a step-by-step synthesis of said different biopolymer probes on said substrate, said plurality of different biopolymer probes comprising a plurality of quality control probes, each quality control probe in said plurality of quality control probes comprising (i) the same predetermined binding sequence or (ii) a different predetermined binding sequence with the same binding specificity, the synthesis of said predetermined binding sequence in each said quality control probe having been initiated during said step-by-step synthesis at sequential cycles of synthesis, wherein each of said quality control probes further comprises a first sequence contiguous with said predetermined binding sequence, wherein at least some of said quality control probes differ from other of said quality control probes in the length of said first sequence, and wherein said first sequence is a sequence of number 0 to N monomers, where N is a whole number equal to or greater than 1, and wherein said sample comprises comprising a binding partner that binds said predetermined binding sequence;

b) detecting or measuring binding between (i) two or more of said quality control probes that differ in the number of said monomers; and (ii) said binding partner in the sample; and

c) comparing binding of said two or more of said quality control probes; wherein if said binding is similar, the absence of a synthesis defect between said sequential cycles of synthesis used to synthesize said two or more quality control probes is indicated.

7. (Currently amended) The method of claim 5 wherein said comparing comprises determining the binding ratio of two of said two or more quality control probes, wherein said binding ratio is the amount of binding of a first of said two quality control probes with said binding partner, divided by the amount of binding of a second of said two quality control probes with said binding partner, and wherein said binding ratio being between 0.5 and 2.0 indicates the absence of said synthesis defect.

8. (Currently amended) The method of claim 6 wherein said comparing comprises determining the binding ratio of two of said two or more quality control probes, wherein said binding ratio is the amount of binding of a first of said two quality control probes with said binding partner, divided by the amount of binding of a second of said two quality control probes with said binding partner, and wherein said binding ratio being between 0.5 and 2.0 indicates the absence of said synthesis defect.

9. (Currently amended) The method of claim 6 further comprising before step (a) ~~the a~~ step of synthesizing said array.

10. (Currently amended) The method of claim 6 wherein said sample comprises (i) total cellular RNA or mRNA from one or more cells or a plurality of nucleic acids derived therefrom, and (ii) said binding partner, wherein said binding partner is not expressed by said one or more cells.

11-36. (Canceled)

37. (Currently amended) The method of ~~any one of claims claim 6, and 34~~ wherein said synthesis defect is a nozzle failure.

38. (Original) The method of claim 37 wherein said array comprises at least a portion of said quality control probes arranged in a periodicity of P and wherein said array is synthesized by step-by-step synthesis using an inkjet printhead with P nozzles, and where P is a whole number equal to or greater than 1.

39. (Original) The method of claim 38 wherein P equals 20.

40. (Currently amended) A method of detecting a nozzle failure using ~~the a~~ positionally addressable array, said method of claim 1 or 2 comprising the following steps in the order stated:

a) contacting ~~the a~~ positionally addressable array of any of claims 1 or 2 with a sample, wherein said positionally addressable array comprises a substrate to which are attached a plurality of different biopolymer probes, said different biopolymer probes being situated at different positions on said substrate and being the product of a step-by-step synthesis of said different biopolymer probes on said substrate, said plurality of different biopolymer probes comprising a plurality of quality control probes, each quality control probe in said plurality of quality control probes comprising (i) the same predetermined binding sequence or (ii) a different predetermined binding sequence with the same binding specificity, the synthesis of said predetermined binding sequence in each said quality control probe having been initiated during said step-by-step synthesis at sequential cycles of

synthesis, wherein said sample comprises ~~comprising~~ a binding partner that binds said predetermined binding sequence, wherein at least a portion of said plurality of quality control probes is arranged in a periodicity of P and wherein said array is synthesized by step-by-step synthesis using an inkjet printhead with P nozzles, wherein P is a whole number equal to or greater than 1;

b) detecting or measuring binding between two or more of said quality control probes and said binding partner in the sample; and

c) comparing binding of said two or more of said quality control probes in a periodicity of P, wherein if said binding is similar, the absence of a nozzle defect is indicated.

41. (Canceled)

42. (Currently amended) The method of claim 5 further comprising before step (a) ~~the a~~ step of synthesizing said array.

43. (Currently amended) The method of claim 5 wherein said sample comprises (i) total cellular RNA or mRNA from one or more cells or a plurality of nucleic acids derived therefrom, and (ii) said binding partner, wherein said binding partner is not expressed by said one or more cells.

44. (Previously presented) The method of claim 5 wherein said synthesis defect is a nozzle failure.

45. (Previously presented) The method of claim 44 wherein said array comprises at least a portion of said quality control probes arranged in a periodicity of P and wherein said array is synthesized by step-by-step synthesis using an inkjet printhead with P nozzles, and where P is a whole number equal to or greater than 1.

46. (Previously presented) The method of claim 45 wherein P equals 20.

47. (New) A method of determining if a positionally-addressable biopolymer array has a synthesis defect, said method comprising the following steps in the order stated:

a) contacting the a positionally-addressable biopolymer array with a sample, wherein said positionally addressable biopolymer array comprises a substrate to which are

attached a plurality of different biopolymer probes, said different biopolymer probes being situated at different positions on said substrate and being the product of a step-by-step synthesis of said different biopolymer probes on said substrate, said plurality of different biopolymer probes comprising a plurality of quality control probes, each quality control probe in said plurality of quality control probes comprising (i) the same predetermined binding sequence or (ii) a different predetermined binding sequence with the same binding specificity, the synthesis of said predetermined binding sequence in each said quality control probe having been initiated during said step-by-step synthesis at sequential cycles of synthesis, wherein the sequence of each quality control probe in said plurality of quality control probes consists of said predetermined binding sequence, and wherein said sample comprises a binding partner that binds said predetermined binding sequence;

- b) detecting or measuring binding between two or more of said quality control probes and said binding partner in the sample; and
- c) comparing binding of said two or more of said quality control probes, wherein if said binding is similar, the absence of a synthesis defect between said sequential cycles of synthesis of said array is indicated.

48. (New) The method of claim 47 further comprising before step (a) a step of synthesizing said array.

49. (New) The method of claim 47 wherein said sample comprises (i) total cellular RNA or mRNA from one or more cells or a plurality of nucleic acids derived therefrom, and (ii) said binding partner, wherein said binding partner is not expressed by said one or more cells.

50. (New) The method of claim 47 wherein said synthesis defect is a nozzle failure.

51. (New) The method of claim 50 wherein said array comprises at least a portion of said quality control probes arranged in a periodicity of P and wherein said array is synthesized by step-by-step synthesis using an inkjet printhead with P nozzles, and where P is a whole number equal to or greater than 1.

52. (New) The method of claim 51 wherein P equals 20.

53. (New) The method of claim 47 wherein said comparing comprises determining the binding ratio of two of said two or more quality control probes, wherein said binding ratio is the amount of said binding partner bound to a first of said two quality control probes, divided by the amount of said binding partner bound to a second of said two quality control probes, and wherein said binding ratio being between 0.5 and 2.0 indicates the absence of said synthesis defect.

54. (New) A method of detecting a nozzle failure using a positionally addressable array, said method comprising the following steps in the order stated:

a) contacting a positionally addressable array with a sample, wherein said positionally addressable array comprises a substrate to which are attached a plurality of different biopolymer probes, said different biopolymer probes being situated at different positions on said substrate and being the product of a step-by-step synthesis of said different biopolymer probes on said substrate, said plurality of different biopolymer probes comprising a plurality of quality control probes, each quality control probe in said plurality of quality control probes comprising (i) the same predetermined binding sequence or (ii) a different predetermined binding sequence with the same binding specificity, the synthesis of said predetermined binding sequence in each said quality control probe having been initiated during said step-by-step synthesis at sequential cycles of synthesis, wherein the sequence of each quality control probe in said plurality of quality control probes consists of said predetermined binding sequence, and wherein said sample comprises a binding partner that binds said predetermined binding sequence, wherein at least a portion of said plurality of quality control probes is arranged in a periodicity of P and wherein said array is synthesized by step-by-step synthesis using an inkjet printhead with P nozzles, wherein P is a whole number equal to or greater than 1;

b) detecting or measuring binding between two or more of said quality control probes and said binding partner in the sample; and

c) comparing binding of said two or more of said quality control probes in a periodicity of P, wherein if said binding is similar, the absence of a nozzle defect is indicated.